

**AMENDMENTS TO THE SPECIFICATION:**

Please replace paragraph [0046] with the following:

This analysis has been used to identify genes that are differentially expressed between normal and dwarf mice and found 46 genes overexpressed in Snell dwarf mice; 49 genes expressed only in Snell mice; 12 genes overexpressed in normal control mice; 13 genes expressed only in normal mice (~~Table 1A-1D in the Appendix~~). Of these selected genes, 71 are previously reported as differentially expressed in Snell dwarf mice, associated with dwarfism, or strongly associated with a similar hormonal status. An additional 10 selections obtained by the new method and not obtained by previous analysis, whose relevance to dwarfism or similar hormonal status are supported by the indicated references, are listed in Table 2. Only genes that passed both criterions (a) standard paired T test (sT-test) with threshold  $p < 0.05$ ; and (b) associative T-test (aT-test) with threshold  $p < 0.005$ ; are presented in Table 2. In addition, this new method was able to more correctly predict the expression levels of 11 genes verified by RT-PCR.